



A  
S  
E  
SEQUENCE LISTING

<110> LITTLE, MELVYN  
KIPRIYANOV, SERGEY  
MOLDENHAUER, GERHARD  
DEUTSCHES KREBSFORSCHUNGSZEUTRUM

<120> MUTATED OKT3 ATIBODY

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<140> 09/424,705

<141> 2000-06-02

<150> PCT/DE98/01409

<151> 1998-05-22

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Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln	
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Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala Ser Val Lys	
30 35 40	

atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac	198
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His	
45 50 55	

tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att	246
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile	
60 65 70	

aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag	294
Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys	
75 80 85	

gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg caa ctg Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu 90 95 100 105	342
agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca aga tat Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr 110 115 120	390
tat gat gat cat tac agc ctt gac tac tgg ggc caa ggc acc act ctc Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu 125 130 135	438
aca gtc tcc tca gcc aaa aca aca ccc aag ctt gaa gaa ggt gaa ttt Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe 140 145 150	486
tca gaa gca cgc gta gat atc gtg ctc act cag tct cca gca atc atg Ser Glu Ala Arg Val Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met 155 160 165	534
tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser 170 175 180 185	582
agt gta agt tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro 190 195 200	630
aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala 205 210 215	678
cac ttc agg ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser 220 225 230	726
ggc atg gag gct gaa gat gct gcc act tat tac tgc cag cag tgg agt Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser 235 240 245	774
agt aac cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asn Arg 250 255 260 265	822
gct gat act gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu 270 275 280	870
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Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly  
35 40 45  
Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly  
50 55 60  
Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr  
65 70 75 80  
Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys  
85 90 95  
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp  
100 105 110  
Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Ser Leu  
115 120 125  
Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Lys Thr  
130 135 140  
Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg Val Asp Ile  
145 150 155 160  
Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys  
165 170 175  
Val Thr Met Thr Cys Ser Ala Ser Ser Val Ser Tyr Met Asn Trp  
180 185 190  
Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr  
195 200 205  
Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser  
210 215 220  
Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala  
225 230 235 240  
Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly  
245 250 255  
Ser Gly Thr Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly  
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His His His  
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<222> (28) ... (897)

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Met Lys Tyr Leu Leu Pro Thr Ala Ala  
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gct ggc ttg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag  
Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln

102

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ctg cag cag tct ggg gct gaa ctg gca aga cct ggg gcc tca gtg aag Leu Gln Gln Ser Gly Ala Glu Ala Arg Pro Gly Ala Ser Val Lys				150
30	35	40		
atg tcc tgc aag gct tct ggc tac acc ttt act agg tac acg atg cac Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr Thr Met His				198
45	50	55		
tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att gga tac att Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile				246
60	65	70		
aat cct agc cgt ggt tat act aat tac aat cag aag ttc aag gac aag Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Asp Lys				294
75	80	85		
gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac atg Asp Lys Ala Thr Leu Thr Asp Lys Ser Ser Thr Ala Tyr Met				342
90	95	100	105	
caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt gca Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala				390
110	115	120		
aga tat tat gat cat tac agc ctt gac tac tgg ggc caa ggc acc Arg Tyr Tyr Asp Asp His Tyr Ser Leu Asp Tyr Trp Gly Gln Gly Thr				438
125	130	135		
act ctc aca gtc tcc tca gcc aaa aca aca ccc aag ctt ggc ggt gat Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly Asp				486
140	145	150		
atc ttg ctc acc caa act cca gct tct ttg gct gtg tct cta ggg cag Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly Gln				534
155	160	165		
agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly				582
170	175	180	185	
gat agt tat ttg aac tgg tac caa cag att cca gga cag cca ccc aaa Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys				630
190	195	200		
ctc ctc atc tat gat gca tcc aat cta gtt tct ggg atc cca ccc agg Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro Arg				678
205	210	215		
ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat cct Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr, Leu Asn Ile His Pro				726
220	225	230		
gtg gag aag gtg gat gct gca acc tat cac tgt cag caa agt act gag Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr Glu				774
235	240	245		

gat ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cg	822
Asp Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala	
250 255 260 265	
gat gct gcg gcc gct gga tcc gaa caa aag ctg atc tca gaa gac	870
Asp Ala Ala Ala Gly Ser Glu Gln Lys Leu Ile Ser Glu Glu Asp	
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<210> 4  
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 Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly  
 35 40 45  
 Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly  
 50 55 60  
 Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr  
 65 70 75 80  
 Asn Tyr Asn Gln Lys Phe Lys Asp Lys Asp Lys Ala Thr Leu Thr Thr  
 85 90 95  
 Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser  
 100 105 110  
 Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr  
 115 120 125  
 Ser Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala  
 130 135 140  
 Lys Thr Thr Pro Lys Leu Gly Gly Asp Ile Leu Leu Thr Gln Thr Pro  
 145 150 155 160  
 Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys  
 165 170 175  
 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr  
 180 185 190  
 Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser  
 195 200 205  
 Asn Leu Val Ser Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly  
 210 215 220  
 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala  
 225 230 235 240  
 Thr Tyr His Cys Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly  
 245 250 255  
 Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Ala Gly Ser  
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gct ggc ttg ctg ctg gca gct cag ccg gcc atg gcg cag gtg cag      102
Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Gln Val Gln
   10          15          20          25

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ctg cag cag tct ggg gct gag ctg gtg agg cct ggg tcc tca gtg aag 150  
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att tcc tgc aag gct tct ggc tat gca ttc agt agc tac tgg atg aac 198  
 Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr Trp Met Asn  
           45                  50                  55

tgg gtg aag cag agg cct gga cag ggt ctt gag tgg att gga cag att 246  
Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Gln Ile  
60 65 70

tgg cct gga gat ggt gat act aac tac aat gga aag ttc aag ggt aaa  
Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe Lys Gly Lys  
75 80 85

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gcc act ctg act gca gac gaa tcc tcc agc aca gcc tac atg caa ctc      342
Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr Met Gln Leu
   90          95          100          105

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agc agc cta gca tct gag gac tct gcg gtc tat ttc tgt gca aga cgg      390
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gag act acg acg gta ggc cgt tat tac tat gct atg gac tac tgg ggt      438  
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                   125                130                135

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Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Lys Leu  
140 145 150

ggc ggt gat atc gtg ctc act cag tct cca gca atc atg tct gca tct 534  
Gly Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser  
155 160 165

cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca agt gta agt 582

Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Val	Ser	
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tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc aaa aga tgg															630	
Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg	Trp	
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att tat gac aca tcc aaa ctg gct tct gga gtc cct gct cac ttc agg															678	
Ile	Tyr	Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Val	Pro	Ala	His	Phe	Arg	
						205				210				215		
ggc agt ggg tct ggg acc tct tac tct ctc aca atc agc ggc atg gag															726	
Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Gly	Met	Glu	
						220				225				230		
gct gaa gat gct gcc act tat tac tgc cag cag tgg agt agt aac cca															774	
Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	
						235				240				245		
ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aac cgg gct gat act															822	
Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Asn	Arg	Ala	Asp	Thr	
						250				255				260		265
gca cca act gga tcc gaa caa aag ctg atc tca gaa gaa gac cta aac															870	
Ala	Pro	Thr	Gly	Ser	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	
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							285									

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							20			25				30		
Leu	Val	Arg	Pro	Gly	Ser	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
							35			40				45		
Tyr	Ala	Phe	Ser	Ser	Tyr	Trp	Met	Asn	Trp	Val	Lys	Gln	Arg	Pro	Gly	
							50			55				60		
Gln	Gly	Leu	Glu	Trp	Ile	Gly	Gln	Ile	Trp	Pro	Gly	Asp	Gly	Asp	Thr	
65							70			75				80		
Asn	Tyr	Asn	Gly	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Glu	
							85			90				95		
Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Ala	Ser	Glu	Asp	
							100			105				110		
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Arg	Glu	Thr	Thr	Thr	Val	Gly	Arg	
							115			120				125		
Tyr	Tyr	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	
							130			135				140		
Ser	Ser	Ala	Lys	Thr	Thr	Pro	Lys	Leu	Gly	Gly	Asp	Ile	Val	Leu	Thr	

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Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met  
            165                    170                    175  
Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln  
            180                    185                    190  
Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu  
            195                    200                    205  
Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser  
            210                    215                    220  
Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr  
            225                    230                    235                    240  
Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr  
            245                    250                    255  
Lys Leu Glu Ile Asn Arg Ala Asp Thr Ala Pro Thr Gly Ser Glu Gln  
            260                    265                    270  
Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser His His His His His His  
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<210> 7  
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*Avail*  
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24